

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 23, 2003, 08:31:36 ; Search time 41.0409 seconds
(without alignments)
431.003 Million cell updates/sec

Title: US-10-077-137-1

Perfect score: 964
Sequence: 1 MLOMAGOCSONEYFDSLHA.....CKSLPALSAITEIKSISAR 184

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	964	100.0	184	S43486	B-cell maturation
2	88.5	9.2	217	C97344	amino acid ABC tra
3	86.5	9.0	858	T08881	prominin - mouse
4	83.5	8.7	1998	T13009	hypothetical prote
5	82	8.5	1009	A57434	protein-tyrosine k
6	81.5	8.5	2233	T28669	surface protein 51
7	81	8.4	773	D89010	protein R08f1.7 l
8	79.5	8.2	1009	S60248	protein-tyrosine k
9	79.5	8.2	1299	T43251	furin (EC 3.4.21.7
10	78.5	8.1	343	D64469	potassium channel
11	78	8.1	841	UC5894	killer cell inhibi
12	77.5	8.0	738	D86345	hypothetical prote
13	77.5	8.0	968	T01733	hypothetical prote
14	77.5	8.0	522	T45824	hypothetical prote
15	77	8.0	539	F72288	hypothetical prote
16	76.5	7.9	357	T21572	hypothetical prote
17	76.5	7.9	1404	T19277	hypothetical prote
18	76	7.9	744	A43353	ascites sialoglyco
19	76	7.9	748	T47250	complex I intermed
20	75.5	7.8	638	T41478	probable transcrip
21	75	7.8	450	B97297	hydrogenase chain
22	75	7.8	857	A41369	S-receptor kinase
23	74.5	7.7	384	S45592	ERD1 protein - yea
24	74.5	7.7	1101	T16840	hypothetical prote
25	74	7.7	377	UC7535	chitinase (EC 3.2.
26	73.5	7.6	307	B95099	membrane protein l
27	73.5	7.6	307	A97967	conserved hypothet
28	73	7.6	304	A89882	hypothetical prote
29	73	7.6	679	B96599	protein P20N2.12 l

ALIGNMENTS

30	73	7.6	733	1	A46373	probable serine/th
31	72.5	7.5	243	2	T31144	hypothetical prote
32	72.5	7.5	408	2	B84518	hypothetical prote
33	72	7.5	416	2	S75097	hypothetical prote
34	72	7.5	855	2	T10665	hypothetical prote
35	71.5	7.4	105	2	T10350	hypothetical prote
36	71.5	7.4	627	2	B71709	conserved hypothet
37	71	7.4	227	2	F72334	hypothetical prote
38	71	7.4	414	2	G71331	probable cell divi
39	71	7.4	473	2	A91207	ABC transporters l
40	71	7.4	480	2	G88690	protein P41H0.1 l
41	71	7.4	500	2	T10543	hypothetical prote
42	71	7.4	660	2	T02768	spike glycoprotein
43	70.5	7.3	188	2	H82933	hypothetical prote
44	70.5	7.3	412	2	T24023	hypothetical prote
45	70.5	7.3	424	2	T14525	S1-locus-specific g

RESULT 1

S43486
B-cell maturation factor - human
N/Alternate names: BCM protein; BCMA protein; BEL protein
C/Species: Homo sapiens (man)
C/Date: 27-Jan-1995 #sequence revision 27-Jan-1995 #text_change 21-Jul-2000
C/Accession: S43486; S31208; S35661
R/Label: Y.; Gras, M.P.; Broet, J.C.; Berger, R.; Larsen, C.J.; Tsapis, A.
Nucleic Acids Res. 22, 1147-1154, 1994
A/Title: The BCMA gene, preferentially expressed during B lymphoid maturation, is bidire
A/Reference number: S43486; MUID:94218335; PMID:8165126
A/Accession: S43486
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-184 <LAA>
A/Cross-references: EMBL:Z29574; NID:G471244; PIDN:CAA82690.1; PID:G471245
R/Label: Y.; Gras, M.P.; Carbonnel, F.; Broet, J.C.; Berger, R.; Larsen, C.J.; Tsapis, A.
EMBO J. 11, 3897-3904, 1992
A/Title: A new gene, BCM, on chromosome 16 is fused to the interleukin 2 gene by a t(4;1
A/Reference number: S31208; MUID:93010984; PMID:1396583
A/Accession: S31208
A/Molecule type: mRNA
A/Residues: 1-184 <LAA>
A/Cross-references: EMBL:Z14954; NID:G29407; PIDN:CAA78679.1; PID:G29408
A/Accession: S36661
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 4-184 <LAA>
A/Cross-references: EMBL:Z14955
C/Genetics:
A/Gene: GDB:BCMA
A/Cross-references: GDB:135977; OMIM:109545
A/Map position: 16p13.1-16p13.1
A/Introns: 44/1; 93/1
C/Superfamily: human B-cell maturation factor

Query Match	100.0%	Score 964;	DB 2;	Length 184;
Best Local Similarity	100.0%	Pred. No. 5.6e-81;		
Matches 184;	Conservative	0;	Mismatches 0;	Indels 0;
			Gaps 0;	
QY	1	MLOMAGOCSONEYFDSLHACIPCOLRCSSNTPPTTCORYCNASVTSNKGNTAILMTCL	60	
DB	1	MLOMAGOCSONEYFDSLHACIPCOLRCSSNTPPTTCORYCNASVTSNKGNTAILMTCL	60	
QY	61	GLSLIISLAVFLVFLFKKISSEPLKDFKNTGSLGGLGMANIDLEKSRGTDEIILPGLLE	120	
DB	61	GLSLIISLAVFLVFLFKKISSEPLKDFKNTGSLGGLGMANIDLEKSRGTDEIILPGLLE	120	
QY	121	YVSECTCEDICIKSKPKVDSDHCPPLPAMEGATITLVTTKNDYCKSLPALSAITEIKS	180	
DB	121	YVSECTCEDICIKSKPKVDSDHCPPLPAMEGATITLVTTKNDYCKSLPALSAITEIKS	180	

QY 181 ISAR 184
181 ISAR 184

RESULT 2

amino acid ABC transporter, permease component CAC3619 (imported) - Clostridium acetobutylicum C97344
C/Species: Clostridium acetobutylicum
C/Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 30-Sep-2001
C/Accession: C97344
R/Molling, J.; Breton, G.; Omeilenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A/Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium C10
A/Reference number: A96900; PMID:21359325; PMID:21359325
A/Accession: C97344
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-217 <KUR>
A/Experimental source: GB:AE001437; PIDN:AAK81542.1; PID:G15026719; GSPDB:GN00168
C/Genetics:
A/Genes: CAC3619
C/Superfamily: histidine permease protein M

Query Match 9.2%; Score 88.5; DB 2; Length 217;
Best Local Similarity 24.8%; Pred. No. 0.98; Indels 65; Gaps 10;
Matches 55; Conservative 25; Mismatches 77;

QY 16 SLHACIPCOLRCSNTPPTTCORCNASV-----TNSVKGNTAI---LMTCLG 62
DB 4 SLSNKVIPVLDDGTRITLLTSSIIIGCIITIMFKTSSVKVNLIGKPYTWLRGT 63
QY 63 SLIISLAIVFV--LMFLRKISSEPLKDEF---KNTGS-----GLGMANIDLEKSR 108
DB 64 PLILQIVYVYVYGGPFLSDKLTMTMPKAAIIGLSNGAVYIAIRIGIILADINGOFEASK 123
QY 109 -----TGDEIILRGLEYTVEEC-----TCEDCI-KSKPKYDSDH 142
DB 124 ALGLTTGQTKRIILPOLNVVIRPCGNERIAMIKOTSLVITMEELKQALLVSSSG 183
QY 143 CPELPAMEGA--TIVTTKTDNYCKSLPAALSAIEIKSIS 182
DB 184 DATVPLVAFGIFFVILITITFTGFSK-----IEKKLS 215

RESULT 3

QY 181 minin - mouse
C/Species: Mus musculus (house mouse)
C/Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C/Accession: T08881
R/Welgmann, A.; Corbell, D.; Hellwig, A.; Hutterer, W.B.
Proc. Natl. Acad. Sci. U.S.A. 94, 12425-12430, 1997
A/Title: Prominin, a novel microvilli-specific polytopic membrane protein of the apical A/Reference number: Z16512; PMID:98024147; PMID:9356465
A/Accession: T08881
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-858 <WEI>
A/Cross-references: EMBL:AF026269; NID:G2559003; PIDN:AB86715.1; PID:G2559004
A/Experimental source: kidney
C/Keywords: glycoprotein; membrane protein

Query Match 9.0%; Score 86.5; DB 2; Length 858;
Best Local Similarity 22.7%; Pred. No. 6;
Matches 44; Conservative 30; Mismatches 67; Indels 53; Gaps 10;

QY 18 LHAICICQLRCSNTPPTTCORCNASVTVSGTALIMTCTGLISLAIVFVLMFL 77
117 LVGCFQCMRC-----CNK-CGGEHQROKONAPCRKKGLSLVILVILMLSGITV 167

QY 78 RKISSEPLKDEFKNTGSLGMANIDLEKSRGD-EIIL---PRGLEYTEECTGE----- 129
DB 168 GFVANQQRTRIKGTQK-----LAKSNRDRQTLTETPKQIDVVEGYTNQKA 218

QY 130 ---DCIKS-----KPVDSHCPPLPAMEGATILVTVK-TNDYCKSLPAL-- 172
DB 219 FSDLDIGISVLGRIRKIDQLKPKV-----TPVLEIRAMATAIKOTDALONMSSLSKS 271

QY 173 ---SATEIEKISIA 183
DB 272 LODAATQLTNTLSS 285

RESULT 4

QY 13009 hypothetical protein T24C20.80 - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 24-Nov-1999
C/Accession: T13009
R/Choisy, N.; Robert, C.; Brotter, P.; Wincker, P.; Cattivico, L.; Artiguenave, F.; Sa submitted to the Protein Sequence Database, July 1999
A/Reference number: Z17586
A/Accession: T13009
A/Molecule type: DNA
A/Residues: 1-1998 <CHO>
A/Cross-references: EMBL:AL096856; GSPDB:GN00061; ATSP:T24C20.80
A/Experimental source: cultivar Columbia; BAC clone T24C20
C/Genetics:
A/Genes: ATSP:T24C20.80
A/Map position: 3
A/Intons: 71/3; 117/1; 162/3; 230/1; 309/3; 348/2; 396/1; 452/3; 532/2; 604/1; 1005/2;
C/Superfamily: Arabidopsis thaliana hypothetical protein T24C20.80

Query Match 8.7%; Score 83.5; DB 2; Length 1998;
Best Local Similarity 29.4%; Pred. No. 27; Indels 43; Gaps 9;
Matches 37; Conservative 18; Mismatches 28;

QY 38 QRYCNASVTVSGTNAIIMTCLGLIISLAIVFVLMFLRKISSEPLKD-EFKN--TGS 94
DB 1089 ERYCGA---NSALGTPSM---C-----SGTGPQDSFEFNSGIP 1122
QY 95 GLGMANIDLEKSRGDEIILPRGLEVYEECTCEDCIKSKP-----KYSDHCPPLPAM 149
DB 1123 SLVKSLSLM--SRIGD-----RGHIFDEGSGCNGRSSAPGLNTGVNIDMCGDL--M 1173
QY 150 EEGAT 155
DB 1174 DGGAT 1179

RESULT 5

QY A57434 protein-tyrosine kinase (EC 2.7.1.112) CAK-beta - rat
N/Alternate names: cell adhesion kinase-beta
C/Species: Rattus norvegicus (Norway rat)
C/Date: 08-Feb-1996 #sequence_revision 08-Feb-1996 #text_change 04-Feb-2000
C/Accession: A57434
R/Sasaki, H.; Nagura, K.; Ishino, M.; Tobioke, H.; Kotani, K.; Sasaki, T.
J. Biol. Chem. 270, 21206-21219, 1995
A/Title: Cloning and characterization of cell adhesion kinase beta, a novel protein-tyro A/Reference number: A57434; PMID:9540356; PMID:7673154
A/Accession: A57434
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-1009 <SAS>
A/Cross-references: GB:D45854; NID:G1000679; PIDN:BA08290.1; PID:G1000680
C/Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo C/Keywords: ATP; phosphotransferase; tyrosine-specific protein kinase
F:423-686/Domain: protein kinase homology <KIN>
F:431-439/Region: protein kinase ATP-binding motif

Query Match 8.5%; Score 82; DB 2; Length 1009;
Best Local Similarity 26.9%; Pred. No. 18;

N/Alternate names: paired basic amino acid cleaving enzyme; proprotein convertase; serin
 C/Species: Spodoptera frugiperda (fall armyworm)
 C/Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 11-Jan-2000
 C/Accession: T43251
 R/Citeplk: M.; Klenk, H.
 submitted to the EMBL Data Library, January 1996
 A/Description: Cloning and functional characterization of FURIN from Spodoptera frugiperda
 A/Reference number: 223368
 A/Accession: T43251
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-1239 <CIB>
 A/Cross-references: EMBL:Z68888; NID:G1167859; PID:e219690; PIDN:CAA93116.1
 A/Experimental source: clone Sfurin 6; ovary
 C/Function:
 A/Description: responsible for the endoproteolytic processing of proproteins with specific
 C/Keywords: hydrolase; serine proteinase

Query Match 8.2%; Score 79.5; DB 2; Length 1299;

Best Local Similarity 24.1%; Pred. No. 40;

Matches 39; Conservative 26; Mismatches 48; Indels 49; Gaps 11;

8 CSQNEFYDSLHACICPCQLRCS-----SNTPLTCQRYCNAS-----VTNSVKGTNAL-W 57

DB 1150 CSRPLRIDILNQCVC-----CSRGVNTNSPTPDC-CHCNPENGECINSSVAGKRIAEW 1205

QY 58 TCGSLGSL-----LISLAV-----FVLMFLRKISSEPLKDEFNKTSGLGGMAN 101

DB 1206 GALTPLPSADAPSVAVVITLAVCAAVGLFTLVLVLAHSPREKTRKTSVNG----- 1259

QY 102 IDLEKSRGTDEILPR-GLGYVEECTCEDCIRKSRVSDH 142

DB 1260 --VEYSR-----LPRTDVDFV-----LNSCTDQDESPVEYH 1289

RESULT 10

D64469

potassium channel homolog - Methanococcus jannaschii

C/Species: Methanococcus jannaschii

C/Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000

C/Accession: D64469

R/Bult: C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, R.; Reich, C.I.; Overbeek, R.; Kirkness, B.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.;

reese, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.;

Science 273, 1058-1073, 1996

A/Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Frazer, C.M.; Smith, H.O.; Woese, C.

A/Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii

A/Reference number: A64300; MUID:96337999; PMID:8688087

A/Accession: D64469

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-343 <BDL>

A/Cross-references: GB:U67575; GB:L77117; NID:G1591992; PIDN:AA99365.1; PID:G1592000; T

C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 17-May-2002

C/Accession: D66345

A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

A/Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A/Reference number: A66141; MUID:21016719; PMID:11130712

QY 153 ATIVTTKTND 163

DB 200 PHILITAKADE 210

RESULT 11

Killer cell inhibitory receptor p91A precursor - mouse

C/Species: Mus musculus (house mouse)

C/Date: 18-Mar-1998 #sequence_revision 18-Mar-1998 #text_change 17-Mar-1999

C/Accession: J05894

R/Yamashita, Y.; Fukuta, D.; Tsuji, A.; Nagabukuro, A.; Matsuda, Y.; Nishikawa, Y.; Ohya

J. Biochem. 123, 358-368, 1998

A/Title: Genomic structures and chromosomal location of p91, a novel murine regulatory r

A/Reference number: J05894; MUID:98218758; PMID:9538215

A/Accession: J05894

A/Status: nucleic acid sequence not shown

A/Molecule type: DNA

A/Residues: 1-841 <YAM>

A/Cross-references: GB:AF040946

C/Comment: This protein function as inhibitory cell-surface molecule against cell activa

C/Genetics:

A/Map position: 7

F/1-23/Domain: signal sequence #status predicted <SIG>

F/24-841/Product: killer cell inhibitory receptor p91A #status predicted <MAT>

F/24-118, 119-220, 221-315, 316-418, 419-517, 518-618/Domain: extracellular Ig-like #status p

F/636-674/Domain: transmembrane #status predicted <TM>

F/675-765/Domain: cytoplasmic #status predicted <CYT>

Query Match 8.1%; Score 78; DB 2; Length 841;

Best Local Similarity 22.7%; Pred. No. 35;

Matches 46; Conservative 32; Mismatches 61; Indels 64; Gaps 9;

9 CSQNEFYDSLHACICPCQLRCS-----SNTPLTCQRYCNASVTNSVKGTNALMTCLGSL 64

DB 598 AQNSFFYLSSASAEVLTVSGPIETSTPPT-----MSMPGLHMYKALIGVSV 649

QY 65 ISLAVFVLMFLL--RKISSEPLKDEFNKTSGLGGMANIDLEKSRGTDEILPRG----- 118

DB 650 AFILFLFILFILRLRRKRGKRDVQEK-----DLQSSGAEFPIRTGELQK 699

QY 119 -----LEYVEECTCEDCIRK-----SKRVSDHCFPLPAMEGATILVTTKTN 162

DB 700 RNPAAQTEGSLVAVSDWQEDGVELNSWTPRED-----PQGT----- 741

QY 163 DYCKSLPAL--SATIEKISNR 184

DB 742 -YAQVPSRLRRKRGVSPVMSR 763

RESULT 12

D66345

hypothetical protein F16F4.10 [imported] - Arabidopsis thaliana

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 17-May-2002

C/Accession: D66345

R/Theologis, A.; Ecker, J.R.; Palm, C.J.; Federapfel, N.A.; Kaul, S.; White, O.; Alonso,

Chen, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;

ansen, N.F.; Hughes, B.; Huizar, L.

A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

A/Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A/Reference number: A66141; MUID:21016719; PMID:11130712

A/Accession: D66345

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-738 <STO>

A/Cross-references: GB:AE005172; NID:G8920639; PIDN:AAF81361.1; GSPDB:GN00141

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